



attachment #4

# SEQUENCE LISTING

<110> BROUN, Pierre  
VAN DE LOO, Frank  
BODDUPALLI, Sekhar  
SOMERVILLE, Chris

<120> PRODUCTION OF HYDROXYLATED FATTY ACIDS IN GENETICALLY  
MODIFIED PLANTS

<130> 20263/255164

<140> 09/117,921

<141> 1999-03-04

<150> 08/597,313

<151> 1996-02-06

<150> PCT/US97/02187

<151> 1997-02-06

<160> 15

<170> MS Word

<210> 1

<211> 543

<212> DNA

<213> Lesquerella fendleri

<220>

<221> UNSURE

<222> 83

<223> any

<400> 1

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attctggtgt taacagttca gtttatcttc ggggtggcctt tgtatctagc ctttaagtga 180
tcaggtagac cttatgatgg ttctgcttca cttttcttcc ctcatgcacc tatctttaag 240
gaccgtgaac gtctccagat atacatctca gatgctggta ttctagctgt ctgttatggg 300
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ttacctcact atgattcaac cgagtgggaa tggattagag gagctttggg tacggtagac 480
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<211> 544

<212> DNA

<213> Lesquerella fendleri

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atcatgatgt taactgtcca gttcgtcttc ggatggccct tgtacttagc cttcaacgtt 180
tctggcagac cctacaatgg ttctgcttcc cttttcttcc ccaatgctcc tatctacaac 240
gaccgtgaac gcctccagat ttacatctct gatgctggta ttctagccgt ctgttatggg 300
ctttaccgtt acgctgttgc acaaggacta gcctcaatga tctgtctaaa cggagtcccg 360
cttctgatag ttaacttttt cctcgtcttg atcacttact tacaacacac tcaccctgcg 420
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ttgcctcact atgattcatc agagtgggat tggcttagag gagcttttagc tactgtagac 480  
 agagactatg gaatcttgaa caaggtgttc cataacatca cagacacca cgtcgcacac 540  
 cact 544

<210> 3  
 <211> 1855  
 <212> DNA  
 <213> *Lesquerella fendleri*

<220>  
 <221> UNSURE  
 <222> 46, 99, 203, 1658, 1788  
 <223> any

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 ttattcatca aataactaaat actacattac ttgttgetgc ctacttctcc tatttcctcc 180  
 gccaccatt ttggaccacag ganccttcca tttaaaccct ctctcgtgct attcaccaga 240  
 agagaagcca agagagagag agagagaatg ttctgaggat cattgtcttc ttcacgttta 300  
 ttaacgtaag ttttttttga ccactcatat ctaaaatcta gtacatgcaa tagattaatg 360  
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 taatggttac cccctcttcc aagaaatcag aaactgaagc cctaaaacgt ggaccatgtg 480  
 agaaaccacc attcactggt aaagatctga agaaagcaat cccacagcat tgtttcaagc 540  
 gctctatccc tcgttctttc tctaccttc tcacagatat cactttagtt tcttgcttct 600  
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 ggctctctta ttgggtatgt caaggctgtg tcttaaccgg tatctgggtc attggccatg 720  
 aatgtggtca ccatgcattc agtgactatc aatgggtaga tgacactgtt ggttttatct 780  
 tccattcctt ccttctcgtc ccttacttct cctggaaata cagtcacgt cgtcaccatt 840  
 ccaacaatgg atctctcag agaatgaag tctttgtccc accgaagaaa gctgcagtca 900  
 aatggtatgt taaataacct aacaaccctc ttggacgcat tctggtgtta acagttcagt 960  
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 aaccggatac ggaacgtggg aagaaagggtg tctactatta caacaataag ttatgaggct 1560  
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 agaagctatg ctttgtttca ataactcag agtccatnta gttgtgttct ggtgcatttt 1680  
 gcctagtatt gtggtgtcgg aagttagtgt tcaaaactgct tcctgctgtg ctgcccagtg 1740  
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 <212> PRT  
 <213> *Lesquerella fendleri*

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Val Lys Asp Leu Lys Lys Ala Ile Pro Gln His Cys Phe Lys Arg Ser  
35 40 45  
Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr Asp Ile Thr Leu Val Ser  
50 55 60  
Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro  
65 70 75 80  
Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr Trp Val Cys Gln Gly Cys  
85 90 95  
Val Leu Thr Gly Ile Trp Val Ile Gly His Glu Cys Gly His His Ala  
100 105 110  
Phe Ser Asp Tyr Gln Trp Val Asp Asp Thr Val Gly Phe Ile Phe His  
115 120 125  
Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg  
130 135 140  
His His Ser Asn Asn Gly Ser Leu Glu Lys Asp Glu Val Phe Val Pro  
145 150 155 160  
Pro Lys Lys Ala Ala Val Lys Trp Tyr Val Lys Tyr Leu Asn Asn Pro  
165 170 175  
Leu Gly Arg Ile Leu Val Leu Thr Val Gln Phe Ile Leu Gly Trp Pro  
180 185 190  
Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala  
195 200 205  
Ser His Phe Phe Pro His Ala Pro Ile Phe Lys Asp Arg Glu Arg Leu  
210 215 220  
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu  
225 230 235 240  
Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr Ala Met Ile Cys Val Tyr  
245 250 255  
Gly Val Pro Leu Leu Ile Val Asn Phe Phe Leu Val Leu Val Thr Phe  
260 265 270  
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Thr Glu Trp  
275 280 285  
Glu Trp Ile Arg Gly Ala Leu Val Thr Val Asp Arg Asp Tyr Gly Ile  
290 295 300  
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His  
305 310 315 320  
Leu Phe Ala Thr Ile Pro His Tyr Asn Ala Met Glu Ala Thr Glu Ala  
325 330 335  
Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr Pro Trp  
340 345 350

Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro  
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Asp Thr Glu Arg Gly Lys Lys Gly Val Tyr Tyr Tyr Asn Asn Lys Leu  
 370 375 380

<210> 5

<211> 387

<212> PRT

<213> Ricinus communis

<400> 5

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Pro Pro Phe Thr Leu Gly Asp Leu Lys Arg Ala Ile Pro Pro His Cys  
 35 40 45

Phe Glu Arg Ser Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val  
 50 55 60

Cys Leu Ser Phe Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr  
 65 70 75 80

Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe  
 85 90 95

Gln Gly Cys Ile Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly  
 100 105 110

His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu  
 115 120 125

Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser  
 130 135 140

His Arg Arg His His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val  
 145 150 155 160

Phe Val Pro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Ser  
 165 170 175

Asn Asn Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu  
 180 185 190

Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp  
 195 200 205

Arg Phe Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg  
 210 215 220

Glu Arg Leu Gln Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr  
 225 230 235 240

Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met  
 245 250 255

Arg Ile Tyr Gly Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met  
 260 265 270  
 Ile Thr Tyr Leu Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser  
 275 280 285  
 Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp  
 290 295 300  
 Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val  
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 Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala  
 325 330 335  
 Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly  
 340 345 350  
 Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe  
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 Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg  
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 Asn Lys Tyr  
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 <212> PRT  
 <213> Arabidopsis thaliana

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 35 40 45  
 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Ser Asp Ile Ile Ile Ala Ser  
 50 55 60  
 Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro  
 65 70 75 80  
 Leu Ser Tyr Leu Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val  
 85 90 95  
 Leu Thr Gly Ile Trp Val Ile Ala His Glu Cys Gly His His Ala Phe  
 100 105 110  
 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser  
 115 120 125  
 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His  
 130 135 140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys  
 145 150 155 160  
 Gln Lys Ser Ala Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu  
 165 170 175  
 Gly Arg Ile Met Met Leu Thr Val Gln Phe Val Leu Gly Trp Pro Leu  
 180 185 190  
 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys  
 195 200 205  
 His Phe Phe Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln  
 210 215 220  
 Ile Tyr Leu Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr  
 225 230 235 240  
 Arg Tyr Ala Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly  
 245 250 255  
 Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu  
 260 265 270  
 Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp  
 275 280 285  
 Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu  
 290 295 300  
 Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu  
 305 310 315 320  
 Phe Ser Thr Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile  
 325 330 335  
 Lys Pro Ile Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr  
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 Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp  
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 Arg Glu Gly Asp Lys Lys Gly Val Tyr Trp Tyr Asn Asn Lys Leu  
 370 375 380

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 <211> 383  
 <212> PRT  
 <213> Brassica napus

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 35 40 45

Ile Pro Arg Ser Phe Ser His Leu Ile Trp Asp Ile Ile Ile Ala Ser  
 50 55 60  
 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro Asn Pro  
 65 70 75 80  
 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val  
 85 90 95  
 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His Ala Ala Phe  
 100 105 110  
 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser  
 115 120 125  
 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His  
 130 135 140  
 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Arg  
 145 150 155 160  
 Arg Ser Gln Thr Ser Ser Gly Thr Ala Ser Thr Ser Thr Thr Phe Gly  
 165 170 175  
 Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu Tyr  
 180 185 190  
 Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala Cys  
 195 200 205  
 His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln  
 210 215 220  
 Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu Leu  
 225 230 235 240  
 Pro Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Leu Arg  
 245 250 255  
 Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr Leu  
 260 265 270  
 Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp  
 275 280 285  
 Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu  
 290 295 300  
 Asn Gln Gly Phe His Asn Ile Thr Asp Thr His Glu Ala His His Leu  
 305 310 315 320  
 Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile  
 325 330 335  
 Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val Val  
 340 345 350  
 Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp  
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 <213> Glycine max

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Phe Ser Leu Ile Ala Trp Pro Ile Tyr Trp Val Leu Gln Gly Cys Leu  
 35 40 45

Leu Thr Arg Val Cys Gly His His Ala Phe Ser Lys Tyr Gln Trp Val  
 50 55 60

Asp Asp Val Val Gly Leu Thr Leu His Ser Thr Leu Leu Val Pro Tyr  
 65 70 75 80

Phe Ser Trp Lys Ile Ser His Arg Arg His His Ser Asn Thr Gly Ser  
 85 90 95

Leu Asp Arg Asp Glu Arg Val Lys Val Ala Trp Phe Ser Lys Tyr Leu  
 100 105 110

Asn Asn Pro Leu Gly Arg Ala Val Ser Leu Leu Val Thr Leu Thr Ile  
 115 120 125

Gly Trp Pro Met Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp  
 130 135 140

Ser Phe Ala Ser His Tyr His Pro Tyr Arg Val Arg Leu Leu Ile Tyr  
 145 150 155 160

Val Ser Asp Val Ala Leu Phe Ser Val Thr Tyr Ser Leu Tyr Arg Val  
 165 170 175

Ala Thr Leu Lys Gly Leu Val Trp Leu Leu Cys Val Tyr Gly Val Pro  
 180 185 190

Leu Leu Ile Val Asn Gly Phe Leu Val Thr Ile Thr Tyr Leu Arg Val  
 195 200 205

His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Lys Gly Ala Leu Ala Thr  
 210 215 220

Met Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His His Ile Thr  
 225 230 235 240

Asp Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His  
 245 250 255

Leu Arg Val Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Asp Thr  
 260 265 270



Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Arg Glu Cys Leu Tyr Val  
 275 280 285

Glu Pro Asp Glu Gly Thr Ser Glu Lys Gly Val Tyr Trp Tyr Arg Asn  
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Lys Tyr Leu Arg Val  
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 <211> 302  
 <212> PRT  
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 35 40 45

Trp Val Val Ala Phe Ser Asp Tyr Gln Leu Leu Asp Asp Ile Val Gly  
 50 55 60

Leu Ile Leu His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr  
 65 70 75 80

Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu  
 85 90 95

Val Phe Val Pro Lys Val Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg  
 100 105 110

Val Leu Thr Leu Ala Val Thr Leu Thr Leu Gly Trp Pro Leu Tyr Leu  
 115 120 125

Ala Leu Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr  
 130 135 140

Asp Pro Tyr Gly Pro Ile Tyr Ser Val Ile Ser Asp Ala Gly Val Leu  
 145 150 155 160

Ala Val Val Tyr Gly Leu Phe Arg Leu Ala Met Ala Lys Gly Leu Ala  
 165 170 175

Trp Val Val Cys Val Tyr Gly Val Pro Leu Leu Val Val Asn Gly Phe  
 180 185 190

Leu Val Leu Ile Thr Phe Leu Gln His Thr His Val Ser Glu Trp Asp  
 195 200 205

Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu  
 210 215 220

Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu  
 225 230 235 240

Phe	Ser	Thr	Met	Pro	His	Tyr	His	Ala	Met	Glu	Ala	Thr	Val	Glu	Tyr
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			260					265					270		
Arg	Glu	Cys	Ile	Tyr	Val	Glu	Pro	Asp	Gln	Ser	Thr	Glu	Ser	Lys	Gly
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Val	Phe	Trp	Tyr	Asn	Asn	Lys	Leu	Ala	Met	Glu	Ala	Thr	Val		
	290					295					300				

Ala Val Ala Phe Gly Leu Tyr Lys Leu Ala Ala Ala Phe Gly Val Trp  
225 230 235 240

Trp Val Val Arg Val Tyr Ala Val Pro Leu Leu Ile Val Asn Ala Trp  
245 250 255

Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu Pro His  
260 265 270

Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala Thr Met  
275 280 285

Asp Arg Asp Tyr Gly Ile Leu Asn Arg Val Phe His Asn Ile Thr Asp  
290 295 300

Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala  
305 310 315 320

Met Glu Ala Thr Lys Ala Ile Arg Pro Ile Leu Gly Asp Tyr Tyr His  
325 330 335

Phe Asp Pro Thr Pro Val Ala Lys Ala Thr Trp Arg Glu Ala Gly Glu  
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Cys Ile Tyr Val Glu Pro Glu Asp Arg Lys Gly Val Phe Trp Tyr Asn  
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Lys Lys Phe  
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<212> PRT  
<213> Ricinus communis

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Pro Tyr Phe Ser Trp Lys His Ser His Arg Arg His His Ser Asn Thr  
35 40 45

Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys Lys Lys Ser Ser  
50 55 60

Ile Arg Trp Tyr Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg Ile Met  
65 70 75 80

Thr Ile Ala Val Thr Leu Ser Leu Gly Trp Pro Leu Tyr Leu Ala Phe  
85 90 95

Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr Asp Pro  
100 105 110

Tyr Gly Pro Ile Tyr Asn Asp Arg Glu Arg Ile Glu Ile Phe Ile Ser  
115 120 125

Asp Ala Gly Val Leu Ala Val Thr Phe Gly Leu Tyr Gln Leu Ala Ile  
 130 135 140  
 Ala Lys Gly Leu Ala Trp Val Val Cys Val Tyr Gly Val Pro Leu Leu  
 145 150 155 160  
 Val Val Asn Ser Phe Leu Val Leu Ile Thr Phe Leu Gln His Thr His  
 165 170 175  
 Pro Ala Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly  
 180 185 190  
 Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe  
 195 200 205  
 His Asn Ile Thr Asp Thr Gln Val Ala His His Leu Phe Thr Met Pro  
 210 215 220

<210> 12  
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 <212> DNA  
 <213> Ricinus communis

<400> 12  
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<210> 13  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: homologous  
 regions of Ricinus communis deduced by hydroxylase  
 sequence and Arabidopsis thaliana deduced desaturase  
 sequence for use as oligonucleotide primer

<400> 13  
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<210> 14  
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<220>  
 <223> Description of Artificial Sequence: homologous  
 regions of Ricinus communis deduced by hydroxylase  
 sequence and Arabidopsis thaliana deduced  
 desaturase sequence for use as oligonucleotide primer

<220>  
 <221> UNSURE  
 <222> 6, 12, 15  
 <223> any

<400> 14  
 taywsncaym gnmgnca yca 20

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regions of Ricinus communis deduced by hydroxylase  
sequence and Arabidopsis thaliana deduced  
desaturase sequence for use as oligonucleotide primer

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<222> 7, 10, 16  
<223> any

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rtgrtgngcn acrtgngtrt c

21